

SEQUENCE LISTING

<110> Genentech, Inc.
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<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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<151> 1999-07-07

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 Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
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 Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
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Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
 180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
 195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
 210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
 225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
 290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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<213> Homo sapiens

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Pro	Tyr	Leu	Gly	Ala	Ile	Cys	Tyr	Cys	Asp	Leu	Phe	Cys	Asn	Arg	Thr

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 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
 180 185

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 19
tgctgtgcta ctccctgcggaa gccc

<210> 20
<211> 24
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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 gaccgaccag ctgagcaggc ggcagatccg cgagttaccaa ctctacagca ggaccagtgg 180
 caagcacgtg caggtcaccg ggcgtcgcat ctccgcccacc gccgaggacg gcaacaagt 240
 tgccaagctc atagtggaga cggacacgtt tggcagccgg gttcgcata aaggggctga 300
 gagtgagaag tacatctgta tgaacaagag gggcaagctc atcgggaagc ccagcgggaa 360
 gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg cttccagaa 420
 cggccggcac gagggttgtt tcatggcatt cacgcggcag gggcgcccc gccaggcttc 480
 cccgagccgc cagaaccagc gcgaggccca cttcatcaag cgcctctacc aaggccagct 540
 gcccctcccc aaccacgccc agaagcagaa gcagttcgag tttgtggct ccccccac 600
 cccgcccggacc aagcgcacac ggccggccca gcccttcacg tagtctgggaa ggcagggggc 660
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 ccccaagccccc ccaaactcctc ctggctagac tgttaggaagg gactttgtt tgtttgggg 1080
 tttcaggaaaa aaagaaaaggg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140
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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

Met	Gly	Ala	Ala	Arg	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Cys	Leu	Gln	Leu
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Leu	Ile	Leu	Cys	Cys	Gln	Thr	Gln	Tyr	Val	Arg	Asp	Gln	Gly	Ala	Met
					20			25					30		

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
					35			40					45		

Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
					50			55					60		

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
					65			70			75		80		

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
					85			90					95		

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
					100			105				110			

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Tyr	Thr
					115			120			125			

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
					130			135			140				

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
					145			150			155		160		

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
					165			170			175				

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
					180			185			190				

Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr		
					195			200			205			

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

cagtagctga gggaccaggcgccatga

28

<210> 25

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 25
ccggtgacct gcacgtgctt gccca 24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<220>
<221> modified_base
<222> (21)
<223> a, t, c or g

<400> 26
gcggatctgc cgccctgctca nctggtcggt catggcgccc t 41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
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aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120
ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
tccagtcat t tgattttgc tggttatttt ttttttctt ttcttttcc caccacattg 240
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
ctttttccct gaagtcttgg cttatcattt coctggggct ctactcacag gtgtccaaac 360
tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420
gcttgacotc agtgcctctt gggatccccg aggvcgttaac cgtactctac ctccacaaca 480
acccaaattaa taatgcttga ttccctgcg aactgcacaa tgtacagtgc gtgcacacgg 540
tctacctgtt tggcaaccaa ctggacaaat tccccatgaa cttcccaag aatgtcagag 600
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tgaagcttga agagctgcac ctggatgaca actccatatic cacagtgggg gtggaaagacg 720
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atctgatcag gctctattt caggacaacc agataaaacca cattccttgc acagccttctt 1080
ccaaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctqactc 1140
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 acgtgcgggg tttcatgtgc caaggtcctg aacaagtccg ggggatggcc gtcaggaaat 1320
 taaatatgaa tctttgtcc tgtcccacca cgaccccccgg cctgcctctc ttccacccag 1380
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 gaagctacac gcetccaaact cctaccacat cggaaacttcc cacgattctt gactggatg 1500
 gcagagaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
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 cctcccgaa gtggaaataac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
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 tcttgcttt ttaaatctt 2479

<210> 28
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 28
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 Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
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 Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
 35 40 45
 Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
 50 55 60
 Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65 70 75 80
 Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
 85 90 95
 Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
 100 105 110
 Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
 115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		
<210> 29		
<211> 21		
<212> DNA		

<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 29	
cggtctacct gtatggcaac c	21
<210> 30	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 30	
gcaggacaac cagataaaacc ac	22
<210> 31	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 31	
acgcagattt gagaaggctg tc	22
<210> 32	
<211> 46	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 32	
ttcacggct gctttgccc agctttgaa gcttgaagag ctgcac	46
<210> 33	
<211> 3449	
<212> DNA	
<213> Homo sapiens	
<400> 33	
acttggagca agccggcgccg gcggagacag aggcagaggc agaagctggg gctccgtcct 60 cgcctccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120	

ctgtagaaca ctggccatag gaaatgtgt tttttgtac tggacttac cttgatata 3360
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggAACAA gttggatttt 3420
 ttatacaata ttaaaattca ccacttcag 3449

<210> 34
 <211> 915
 <212> PRT
 <213> Homo sapiens

<400> 34
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 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
 20 25 30
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
 35 40 45
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
 50 55 60
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
 65 70 75 80
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
 85 90 95
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
 100 105 110
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
 115 120 125
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
 130 135 140
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
 145 150 155 160
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
 165 170 175
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
 180 185 190
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
 195 200 205
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
 210 215 220
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245		250	255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260		265	270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280		285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295		300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325		330	335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340		345	350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355		360	365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370		375	380
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405		410	415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420		425	430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435		440	445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450		455	460
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485		490	495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500		505	510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815

 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830

 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845

 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860

 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880

 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895

 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910

 Arg Tyr Arg
 915

 <210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 35
 gtgaccctgg ttgtgaatac tcc 23

 <210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 36
 acagccatgg tctatagtt gg 22

 <210> 37
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 37
 gcctgtcaagt gtccctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38
 <211> 1813
 <212> DNA
 <213> Homo sapiens

<400> 38
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 gggccatgtat ttccctcccg gggccctgg tgaccaactt gctgcggttt ttgttcctgg 180
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 ggttgcaggc ggtggaggaa ggggaagtgg tgcttccagc gtggtagcacc ttgcacgggg 300
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 aaaaggagga tcaggtgttg tccatcatca atggggtcac aacaagcaaa cctggaggat 420
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 gtctccaggg tggcccccattt gttggggcaa acgtgaccct gagctgcccag tctccaaggaa 660
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<210> 39
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 <212> PRT
 <213> Homo sapiens

<400> 39
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20	25	30	
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
370 375 380

Gln Ala Gly Ser Leu Val
385 390

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<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 40
agggtctcca ggagaaaagac tc

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<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 41
attgtgggcc ttgcagacat aqac

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<210> 42
<211> 50
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 42		
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<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtgggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
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<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
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cagcagcttc agccaccagg agtgg		25
<210> 46		
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oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		

<211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 47
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 <210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

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 tcacaattt tgaagatgtt aatgtatgtt gaaattttaac tcagtcctgt ggcggaaat 240
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 caaactgcca ttttagataat gtctgtatag ctgcaaaatataat ttaacaaaaaa 420
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aa						2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
 35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
 130 135 140

Glu	Val	Tyr	Arg	Asn	Ser	Val	Thr	Asp	Leu	Ser	Pro	Thr	Asp	Ile	Ile
145					150					155					160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (61)

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<223> a, t, c or g

<400> 50
tggaaacata tcctccctca tatgaatatg gatggagact acataaatat attccaaag 60
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aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccacccacat tataatgaaact tgaaaaaata acatttacat taagtcatcg aaaggtcaca 300
gataaggata ggagtctatg tggatTTTg gaataactcac ctgataaccat gaatggcagc 360
tggcttcag agggctgtga gctgacatac tcaaattgaga cccacacccatc atgccgctgt 420
aatcacctga cacatTTGc aattttgatg tcctctggtc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 51
ggtaatgagc tccattacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 52
ggagtagaaaa ggcgcattgg 18

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 53
cacctgatac catgaatggc ag 22

<210> 54
<211> 18
<212> DNA

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<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 54	
cgagctcgaa ttaattcg	18
<210> 55	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
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<400> 55	
ggatctcctg agtcagg	18
<210> 56	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 56	
cctagtttag tgatccttgt aag	23
<210> 57	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 57	
atgagaccca cacctcatgc cgctgtataatc acctgacaca ttttgcatt	50
<210> 58	
<211> 2137	
<212> DNA	
<213> Homo sapiens	
<400> 58	
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 gaggttgcgtt ttgtatatta aaatggatgt ttgtttgtt 2137

<210> 59
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Arg Ser Gly Cys Val Val Val His Val Val Trp Ile Leu Ala Gly Leu
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
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Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtgtt

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62
 ccagtccggc gacaagccca aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
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 gctgctgctg cgctacctgg tggtcgcctt gggctatcat aaggcctatg ggttttctgc 180
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 ttcaatatac cggatcaaaa atgtgacaag aagtgtatgc gggaaatatc gttgtgaagt 420
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtactc tggaaagtatt 480
 agtggctcca gcagttccat catgtgaagt accctttct gctctgagtg gaactgtgg 540
 agagctacga tgtcaagaca aagaaggaa tccagctcct gaatacacat gtttaagga 600
 tggcatccgt ttgctagaaa atcccaact tggctcccaa agcacaaca gctcatacac 660
 aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
 atattccctgt gaagcccgca attctgttgg atatcgagg tgcctggaa aacgaatgca 780
 agtagatgtat ctcaacataa gtggcatcat agcagccgtt gtagtgtgg ccttagtgat 840
 ttccgtttgt ggccttgggtg tatgctatgc tcagaggaaa ggctacttt caaaagaaac 900
 ctccctccag aagagtaatt ctcatctaa acccacgaca atgagtgaaa atgtgcagtg 960
 gctcacgcct gtaatcccag cactttggaa ggcgcggcg ggcggatcac gaggtcagga 1020
 gttctagacc agtctggcca atatggtaa accccatctc tactaaaata caaaaattag 1080
 ctgggcattgg tggcatgtgc ctgcagttcc agtgcgttgg gagacaggag aatcacttga 1140
 accccggagg cggaggttgc agtgcgtga gatcacgcca ctgcagttcc gcctggtaa 1200
 cagagcaaga ttccatctca aaaaataaaaa taaataaata aataaataact gtttttacc 1260
 tgtagaattt ttacaataaa tatagtttg tattc 1295

<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45

 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60

 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80

 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95

 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110

 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125

 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140

 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160

 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175

 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190

 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205

 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220

 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240

 Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255

 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270

 Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

<210> 65
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 65
 atcgttgtga agtttagtgcc cc 22

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 66
 acctgcgata tccaaacagaa ttg 23

<210> 67
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67
 ggaagaggat acagtcaactc tggaagtatt agtggctcca gcagttcc 48

<210> 68
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 68
 gacatcgag gtgggctagc actgaaaactg ctttcaaga cgaggaagag gaggagaaaag 60
 agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120
 gcatcatgct gctattcctg caaatactga agaaggcatgg gatttaataa ttttacttct 180
 aaataaaatga attactcaat ctcctatgac catctataca tactccacct tcaaaaaagta 240
 catcaatatt atatcattaa ggaaatagta accttcttctt ctccaatatg catgacattt 300
 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360
 tggcattcat catttgacaa atgcaagcat cttccttatac aatcaagctcc tattgaactt 420
 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtac 540

aagctgtaga taaaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccatttgt 600
 ttacaccagg atccatttat atggaagcat ctacagtggta ttgtaatgtat ttaggtctt 660
 taacttccc agccagattt ccagctaaca cacagattct ttccttacag actaacaata 720
 ttgcaaaaat tgaataactcc acagacttcc cagtaaacct tactggcctg gatttatctc 780
 aaaacaattt atcttcagtc accaatatta atgtaaaaaaaa gatgcctcag ctcccttctg 840
 tgtacccatggaa gaaaaacaaa cttactgaac tgccctgaaaaa atgtctgtcc gaactgagca 900
 acttacaaga actcttatatt aatcacaact tgcttctac aatttcaccc ggagccctta 960
 ttggccatca taatcttctt cgacttcatc tcaattcaaa tagattgcag atgatcaaca 1020
 gtaagggtt tgatgtctt ccaaatacttag agattctgtat gattggggaa aatccaattt 1080
 tcagaatcaa agacatgaac tttaaggcctc ttatcaatct tcgcgcctg gttatagctg 1140
 gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200
 tctcttttgcataacagg cttattaaag taccatgtat tgctcttcaa aaagttgtaa 1260
 atctcaattt ttggatcta aataaaaatc ctattaaatag aatacgaagg ggtgatttta 1320
 gcaatatgct acacttaaaaa gagttggggaa taaataatgcgcctgatcg atttccatcg 1380
 atagtcttgc tggtggataac ctgccatggatt taagaaaaat agaagctact aacaacccta 1440
 gattgtcttgcataaccccc aatgcatttt tcagactccc caagctggaa tcactcatgc 1500
 tgaacagcaa tgctctcagt gccctgtacc atggtaccat tgagtctctg ccaaaccctca 1560
 agggaaatcag catCACAGT aaccccatca ggtgtactg tgcattccgt tggatgaaca 1620
 tgaacaaaac caacattcga ttcatggagc cagattcact gtttgcgtg gaccacccctg 1680
 aattccaaagg tcagaatgtt cggcaagtgc atttcaggaa catgtggaa atttgcgtcc 1740
 ctcttatagc tcctgagagc ttcccttcta atctaaatgt agaagctggg agctatgtt 1800
 ccttcactg tagagctact gcagaaccac agcctgaaat ctactggata acacccctcg 1860
 gtcaaaaaact ctgcctaat accctgacag acaagttcta tgccattctt gaggaaacac 1920
 tagatataaa tggcgttaact cccaaagaag ggggttata tacttgtata gcaactaacc 1980
 tagttggcgc tgacttgaag tctgttatga tcaaaatgtt gggatctttt ccacaagata 2040
 acaatgctc tttgaatatt aaaataaagag atattcaggc caattcagtt tggtgtcct 2100
 ggaaagaag ttctaaaattt ctcaaatcta gtgtttaatgg gacaggctt gtcaagactg 2160
 aaaattctca tgctgcgcaaa agtgcctgaa taccatctgtatcaaggta tataatctta 2220
 ctcatctgaa tccatcaact gaggataaaa ttgttatgtatccaccatctatcaga 2280
 aaaacagaaaaaaaatgtgtta aatgtcacca coaaagggtt gcaccctgtat caaaaagagt 2340
 atgaaaaagaa taataccaca acacttatgg cctgtcttgg aggccctctg gggattattg 2400
 gtgtgatatg tcttatcagc tgcctcttc cagaaatgaa ctgtgatggt ggacacagct 2460
 atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat ctcctctgaa 2520
 taaatctctg ggaagcagga aaagaaaaaa gtacatcaact gaaagttaaa gcaactgtt 2580
 taggttacc aacaaatatgt tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

<210> 69
 <211> 708
 <212> PRT
 <213> Homo sapiens

<400> 69
 Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
 1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
 50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

4

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
 625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
 645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
 660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
 675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
 690 695 700

Thr Asn Met Ser
 705

<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens

<400> 70
gcccgggact ggccgaagg gcccaagcaa gaaaagaaaat aatgaagaga cacatgtgtt 60
agctgcagcc ttttggaaaca cgcaagaagg aaatcaatag tggacagg gctggAACCT 120
ttaccacgct tggagta gatgagaat ggctcgta ttatgtcac attccagcat 180
aatctggta gacctgtgtt taacccgttc cctctccatg tggatctcc tacaaagttt 240
tgttcttatg atactgtgtt ttcattctgc cagttatgtt cccaaGGGCT gtctttgttc 300
ttcctctggg ggtttaatg tcacctgttag caatgcAAAT ctcaaggAAA tacctagaga 360
tcttcctctt gaaacagtct tactgtatct ggactccaat cagatcacat ctattccaa 420
tggaaatttt aaggacctcc atcaactgag agttctcaac ctgtccAAA atggcattga 480
gtttatcgat gagcatgcct tcaaaggAGT agctgaaACC ttgcagactC tggacttGTC 540
cgacaatcggtt attcaaagtgt tgccatgttcaat aacctgtagg ccaggGCCAG 600
aattgccaac aaccctggc actgcgactg tactctacag caagtctga ggagcatggc 660
gtccaatcat gagacagccc acaacgtgat ctgtAAAAGC tccgtttgg atgaacatgc 720
tggcagacca ttctcaatg ctgcacatcg cgtgcacCCt tggatctcc ctaaaaaAAAC 780
taccgattat gccatgtgtt tcaccatgtt tggatgttcc actatgggtga tctcatatgt 840
ggtatattat gtgaggcAAA atcaggagga tgccggaga cacctcgaaat acttggAAATC 900
cctgccaAGC aggcaAGA aagcagatga acctgtatgtt attagcactg tggatAGTG 960
tccaaACTGA ctgtcattGA gaaAGAAAGA aagtatTTG cgattgcAGT agaaATAAGT 1020
ggtttacttc tcccatccat tggatgttcaat tggatgtt tttttGAAT 1080
tatgccactg ctgaaACTTTT aacAAACACT acaacataAA taatttgagt ttaggtgatC 1140
cacccttAA ttgtacCCC gatggatata ttctgagtaa gctactatct gaacattAGT 1200
tagatccatc tcactatttA ataatgaaat ttatTTTTT aattaaaAG caaataAAAG 1260
cttaactttg aaccatgggA aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71
<211> 259
<212> PRT
<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255

Thr Val Val

<210> 72
 <211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

accgagccga gcggaccgaa ggccgcggcc agatgcaggt gagcaagagg atgctggcg 60
 gggcggtgag gacatgccc agccccctcc tggcctgtcg gcagccatc ctccctgtgg 120
 tgctgggctc achtgtgtca ggctcgccca cgggctgccc gccccgtgc gagtgctccg 180
 cccaggaccg cgctgtgtcg tgccaccgca achtgtttgt ggcagtcccc gagggcatcc 240
 ccaccggagac ggcgcgtgtg gacctaggca agaaccgcat caaaaacgctc aaccaggacg 300
 agttcggccag cttcccgac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
 tggagcccg cgccctcaac aacctttca acctccggac gctgggtctc cgcagcaacc 420
 gcctgaagct catcccgcta ggcgttca ctggcctca gAACCTGACC aagcaggaca 480
 tcagcgagaa caagatcggtt atcctactgg actacatgtt tcaggacatc tacaacactca 540
 agtcacttgg agttggcgac aatgacactcg tctacatctc tcaccgcgc ttcagcgcc 600
 tcaacagcct ggagcagctg acgctggaga aatgcaacct gacccatc cccaccgagg 660
 cgctgtccca cctgcacggc ctcatcgatc tgaggctccg gcacctaacc atcaatgcca 720
 tccgggacta ctccctcaag aggctgtacc gactcaaggt cttggagatc tcccactggc 780
 cctacttgg a cccatgaca cccaaactgccc tctacggcct caacctgacg tccctgtcca 840
 tcacacactg caatctgacc gctgtgcctt acctggccgt cggccaccta gtctatctcc 900
 gcttcctcaa ccttccttac aaccccatca gcaccattga gggctccatg ttgcatgagc 960
 tgctccggct gcaggagatc cagctgggtt gccccggcgc ggcgtgggtt gagccctatg 1020
 cttcccgccg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
 tggaggaatc achtttccac tcgggtggca acctggagac actcatctg gactccaacc 1140
 cgctggcctg cgactgtcggtt ctccctgtggg tttccggcg cggctggcggtt ctcaacttca 1200
 accggcagca gcccacgtgc gccacggccg agtttgtcca gggcaaggag ttcaaggact 1260
 tccctgtatgt gctactgccc aactacttca cctgcgcggc cggccacatc cgggaccgca 1320
 aggcccagca ggtgtttgtt gacgaggggcc acacgggtca gtttgtgtc cgggcccgtt 1380
 gcgaccggcc gcccgcatac ctctggctt caccggaaa gcacctggtc ttagccaaga 1440
 gcaatggcg gtcacagtc ttccctgtatgc acacgggtca ggtgcgtac gcccaggatc 1500
 aggacaacgg cacgtacctg tgcatcgccg ccaacggggg cggcaacgac tccatgccc 1560
 cccacctgca tgcgtcgccg tactcgcccg actggccca tcagccaaac aagaccttc 1620
 ctttcatctc caaccagccg ggcgaggggag aggccaacag caccggcc actgtgcctt 1680
 tcccttcga catcaagacc ctcatcatcg ccaccacat gggcttcatc tctttctgg 1740
 gctcggtcctt cttctgcctg gtgctgtgt ttctctggag cggggcaag gcacacacaa 1800
 agcacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggatc agctccggcc 1860
 acgcgcggccg caagttcaac atgaagatga tatgaggccg gggcgggggg cagggaccac 1920
 cggggggccg ggcaggggaa ggggcotggc cgccacctgc tcacttcca gtccttccca 1980
 ccttcctccctt acccttctac acacgttctc ttttcctctc cggccctccgtt cccctgtgc 2040
 ccccccggccag ccctcaccac ctgccttcct tctaccagga cctcagaagc ccagacctgg 2100
 ggaccccccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
 ggcagagtca ataattcaat aaaaaagttt cgaactttctt ctgttaacttgc gtttcaata 2220
 attatggatt tttatgaaaaa cttgaaataa taaaaaagaga aaaaaactaa aaaaaaaaaa 2280
 aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
 20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605
Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile		
610	615	620

<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 74
tcacctggag cctttattgg cc 22

<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 75
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<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 76
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gg 52

<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 77	
ccatgtgtct cctcctacaa ag	22
<210> 78	
<211> 23	
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<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 78	
gggaatagat gtgatctgat tgg	23
<210> 79	
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<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
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<400> 79	
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<210> 80	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 80	
agcaaccgcc tgaagctcat cc	22
<210> 81	
<211> 24	
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<213> Artificial Sequence	
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oligonucleotide probe	
<400> 81	
aaggcgccgt gaaaagatgt a gacg	24
<210> 82	

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 82
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<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

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 agccaggggag cccggccggga agcgcgatgg ggccccccagc cgcctcgctc ct当地
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 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagttc acctgctcaa 480
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

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Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
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Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
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Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

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22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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<400> 87
cctagcacag tgacgaggga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 88
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

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<210> 91
 <211> 696
 <212> PRT
 <213> Homo sapiens

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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr 35 40 45
Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe 50 55 60
Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn 65 70 75 80
Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
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Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
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 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
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 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
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 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
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 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
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 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
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 625 630 635 640
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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 <213> Homo sapiens

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Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
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Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

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370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
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Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
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oligonucleotide probe		
<400> 102		
acagctccccg attcagttt cttgcatacg ggacgaaatc ggcgctcgct		50
<210> 103		
<211> 2026		
<212> DNA		
<213> Homo sapiens		

<400> 103

ggacgcgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca gggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg ctcgcctt gccggccgcg 120
tatcccccg ctacctggc cgccccggg cggtgccgc gtgagaggga gcgcgcggc 180
agccgagcgc cggtgtgagc cagcgtctgc gccagtgtg gcccgggtg gagcgcgggtg 240
ggtgtggagg ggcgtgtgtg cggcgccgcg cggctgggg tgcaaaccgg gacgtctac 300
gctgccatga gggcgccgaa cgcctggcg coactctgoc tgctgtggc tgccgcccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgtttca catgtgttgg cattcttact 420
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tgtacttggaa aatcacagt tcccgaagga aaagttagtgc ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgcgcstat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg ctctgtggc acyttccggc ctggagccct tgggtccagt 660
ggcaacaaga tggatggcga gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
gccatgttct cggctgtga accaaacgaa agaggggatc agtattgtgg aggactccct 780
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aagtttgatg tggagcggaga taactactgc cgatatatgatt atgtggctgt gtttaatggc 960
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gtgttatttgc tttcaccttc aagccttgc cctgaggtgt tacaatcttgc tcttgcgtt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
 20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
 50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350	
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro			
355	360	365	
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu			
370	375	380	
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys			
385	390	395	400
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys			
405	410	415	

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105
ccgattcata gacctcgaga gt

22

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106
gtcaaggagt cctccacaat ac

22

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108
<211> 1838
<212> DNA

<213> Homo sapiens

<400> 108

cgacgcgtg ggccggacgcg tggcggcccc acggcgcccc cgggctgggg cggtcgcttc 60
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aagggcctag tcccgactgt gctctggggc ctcagccctct tcctcaacct cccaggac 180
atctggctcc agccctctcc acctccccag tcttctcccc cgcctcagcc ccatccgtgt 240
catacctgcc ggggactggg tgacagctt aacaaggccc tggagagaac catccggac 300
aactttggag gtggaaacac tgcctgggg gaagagaatt tgtccaaata caaagacagt 360
gagaccggcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
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gccccggacc tctccagtg gctgtgctca gattccctga agctctgctg ccccgccaggc 540
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tacgggggtg aggccctgtgg ccagtgtggc ctggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgtttggc ccctgtgccc gatgctcagg acctgaggaa 780
tcaaactgtt tgcataatgcaaa gaagggtctgg gccctgcattt acctaagtgt tgtagacatt 840
gatgagtggtg gcacagaggg agccaaactgt ggagctgacc aattctgcgtt gaacacttag 900
ggctccatg agtgcggaga ctgtgcctaa gctgcctag gctgcattggg ggcaggccca 960
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gatgagtggtg agacagaggt gtgtccggga gagaacaacg agtgtaaaaa caccgaggc 1080
ggttatcgct gcatctgtgc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccgag agtcagcagg ctcttcctca gagatgacaa aagacgagggt ggtggctgt 1200
cagcagatgt tctttggcat catcatctgt gcaactggcca cgctggctgc taagggccac 1260
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gagcgcagtg accgtgtgt ggagggttcc atcaagggca gataatcgcg gccaccac 1380
gttaggaccc tccccaccca cgctggcccc agagcttggg ctgcctact gctggacact 1440
caggacagct tggtttattt ttgagagtg ggtaaggcacc cctacgtgcc ttacagagca 1500
gcccaggatcc ccaggccccgg gcagacaagg cccctgggg aaaaagttagc cctgaagggt 1560
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acaggggtgg ggccatcaca gtcctccctt gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac cccattgcca ctatatttattt catctcaggaa aataaaagaaa 1800
ggtcttgaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
 20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
405 410 415

Ile Lys Gly Arg
420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

112

atctgcttgc agccctcggt ac

22

113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113
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 cagcacatg cagcccgtgt ggctctgctg ggcactctgg gtgttgcggc tggccagccc 120
 cggggccgccc ctgaccgggg agcagctctt gggcagcctg ctgcggcagc tgcagctcaa 180
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcatcccca cccacgttag 240
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcc gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360
 gctggtgttc ggcattggago agcggctgcc gccaaacagc gagctgtgc aggccgtgt 420
 gcccgtcttc caggagccgg tccccaaaggc cgcgtgcac aggacacgggc ggctgtcccc 480
 ggcgcagcgcc cgggccccggg tgaccgtcga gtggctgcgc gtcccgacg acggctccaa 540
 ccgcacccctcc ctcatcgact ccaggctggt gtccgtccac gagacggcgt gqaaggcctt 600
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 ggtccgttt gcctcgcagg gggcgcacgc cgggcttggg gagcccccagc tggagctgca 780
 caccctggac ctggggact atggagctca gggcgactgt gacccctgaag caccaatgac 840
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 cgagaactgg gtgctggagc ccccggcgtt cttggcttat gagtgtgtgg gcacctgccc 960
 gcagcccccg gaggccctgg cttcaagtgc gccgtttctg gggcctcgac agtgcatacg 1020
 ctcggagact gactcgctgc ccatgatcgat cagcatcaag gaggaggcga ggaccaggcc 1080
 ccagggtgtc agcctgccc acatgagggt gcagaagtgc agctgtgcct cggatgggtc 1140
 gctcgtgcca aggaggctcc agccataggc gcctagtgtta gccatcgagg gacttgactt 1200
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 acctgagggc agaaaagccc ntgtgtcatt gtttacttgt cctgtcactg gatctgggt 1500
 aaagtccctcc accaccactc tggacctaag acctgggtt aagtgtgggt tgcgtcatccc 1560
 caatccagat aataaaagact ttgtaaaaaca tgaataaaaac acattttattt ctaaaa 1616

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1 5 10 15

Ser	Pro	Gly	Ala	Ala	Leu	Thr	Gly	Glu	Gln	Leu	Leu	Gly	Ser	Leu	Leu
20													30		

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

aatcctgtga agttgtcctg tgcctactcg ggctttctt ctccccgtgt ggagtggaaag 240
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 gaggaccggg tgacccctt gccaactggg atcacccatca agtccgtgac acgggaagac 360
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 gtcaagctca tcgtgcttgc gcctccatcc aaggctacag ttaacatccc ctccctgtcc 480
 accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
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 agcaactctt cctatgtcct gaatccaca acaggagac tggctttga tcccctgtca 660
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 tcaaataatgtg tgcgcatgga agctgtggag cgaatgtgg gggatcgatcg ggcagccgtc 780
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<210> 119
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 119 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile 1 5 10 15
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His 20 25 30
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu 35 40 45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe 50 55 60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr 65 70 75 80
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

tgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgggtgcct 50

<210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctgggtt caaaagatggg 20

<210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgcgtgaaggc acgg 24

<210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact cagggtgtac 20

<210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

```

<400> 125
actcagcagt ggttagaaag 20

<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 126
cagcgcgtgg ccggcgccgc tgggggaca gatgagcgg cggtggatg gcgcagggtt 60
gagcggtggcg aacaggggct ctgggctgg cgctgctgct gtcgtcgcc ctcggactag 120
gcctggaggc cggcgagc ccgcttcca cccgcaccc tgcccaggcc gcaggcccc 180
gctcaggctc gtgcccaccc accaagtcc agtgcgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gaagcgatgg cagcgatgag gaggagtgca 300
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gcacccggcgt cagtactgc tctggggaa ctgacaagaa actgcgcac tgcagccgc 420
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tcacctctc caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtccct 660
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aagttgttc 1210

<210> 127
<211> 282
<212> PRT
<213> Homo sapiens

<400> 127
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80

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Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 128
 aagttccagt gccgcaccag tggc

<210> 129

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 129
ttggttccac agccgagctc gtcg                                24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaaggcc aatgccacc      50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cggctctcgct cgctcgcgca gcggcgccag cagaggcgc gcacagatgc 60
gggttagact ggcgggggga ggaggccggag gagggaaagga agctgcattgc atgagaccca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaacccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgtatcctg tggtttccgc tggcgcgtgtg ctgcgcct gcacagctca 300
cgggcggtt cgatgacctt caagtgtgtg ctgaccccg cattcccgag aatggcttca 360
ggaccccccag cggagggggtt ttctttaag gctctgttagc ccgatattcac tgccaagacg 420
gattcaagct gaaggccgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcagaaga ttgcgttatac cctcaaatacg 540
aagatgtca gattcataac aagacatata gacatggaga gaagctaatac atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcttta tgcgcgtatg 660
atgaaacgtg gaataatctg cccatctgtc aaggctgcct gagacccctta gcctcttata 720
atggctatgt aaacatcttct gagctccaga cctcccttccc ggtggggact gtgtatcttcc 780
atcgctgttt tcccggtttt aaacttgcgtg ggtctgcgtta ttcttgatgtc ttacaaaacc 840
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accaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaagatt gtggcggttca 1140

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cggcaaccag tggctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
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 ctccccagggtg ccaagagagc acccaccctg ctccggacaa ccctgacata attgccagca 1560
 cggcagagga ggtggcatcc accagccccg gcatccatca tgcccactgg gtgttggcc 1620
 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
 gttgatctgt ggagttgatt ccttccttc tcttggttt agacaatgt aaacaaagct 1740
 ctgatcctta aaattgctat gctgatagag tggtgaggcc tggaaagcttg atcaagtcct 1800
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1															15

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
20														30

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
35															45

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
50															60

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65															80

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
85															95

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
100															110

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
115															125

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
130															140

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145															160

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
165															175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133
atctcctatc gctgcttcc cggt 23

<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134
agccaggatc gcagtaaaac tcc 23

<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens

<400> 136
cccacgcgtc cgctccgcgc cctccccccc gactcccgtg cggtcgtcg gtggcctaga 60
gatgtgtctg ccgcgggtgc agttgtcgcg cacgcctctg cccgcgcagg cgctccaccg 120
ccgttagcgcc cgagtgtcg ggccgcgcacc cgagtccggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgtggcc gtgctgtcg tgccgtcgcc ggccgcgcacg ggtcgccctgc 240
tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgcggggga gggacacaga 300

ggccttgta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agcttagtcag catcgagtct gaagatgaac 420
agaaaactgat agaaaagttc attgaaaacc tttgccatc tgatgggtac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
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acatgttcca gtggaatgtat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt cttcttagag aagctgaagg tgagggaaaca gagctgacaa 780
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gagaagctgc cttaatctg gcctacatcc taatccccag cattccctt ctctctctcc 900
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tccagctcga ccttatgaga aggtacctt cccaggtctg gcacatagta gagtctcaat 1560
aatgtcact tgggtgggtt tatctaactt ttaagggaca gagctttacc tggcagtgt 1620
aaagatgggc tggagactt ggaaaaccac ctctgttttc cttgcctat acagcagcac 1680
atattatcat acagacagaa aatccagaat ctttcaaaag cccacatatg gtgcacagg 1740
ttggcctgtg catcgcaat tctcatatct gttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
 100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 138
gttcattgaa aaccttgc catctgatgg tgacttctgg attggctca      50

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 139
aagccaaaga agcctgcagg aggg      24

<210> 140
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 140
cagtccaagc ataaaggc tggc      24

<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 141
gggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaagg ctggatgtac 60
gcattcccgag gttcccgccg acttgggggc gccccctgag ccccgccgccc cgccagaagac 120
tttgtttgc ctccctgcgcg ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
tggtgtgttc agcatgcgcgct tgtggacccc agtggggcgtc ctgacactcg tggcgtactg 240
cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300
cgaccgcagc ctgctgaagt tgaaaatggt gcagggtcggt ttgcacacg gggctcgag 360
tcctctcaag ccgctccgc tggaggagca ggttagagtgg aaccccccacg tattagagg 420
cccaccccaa actcagtttgc attacacagt caccaatcta gctgggtggc cgaaaccata 480
ttctccttac gactctcaat accatgagac caccctgaaag gggggcatgt ttgctggca 540
gctgaccaag gtgggcattgc agcaaatgtt tgccctggga gagagactga ggaagaacta 600
tgtgaaagac attcccttgc ttccaccaac ctcaacccca caggaggtat ttattcggtc 660
cactaacatt ttccgaaatc tggagttccac ccgttgtttgc ctggctggca tttccagtg 720

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tcgaaaagaa ggaccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
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tttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
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agttggaaat gaagagtaac tgatttataa aagcaggatg tggatgttt aaaataaaagt 1500
gcctttatac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 143
ccaaactacca aagctgctgg agcc                                24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 144
gcagcttat taccacggga agga                                24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 145
tccttcccggt ggtaatagag ctgc                                24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg      45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttcttagc 60
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

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gggcctccac cgctgtgaag ggccgggtgga ggttggAACAG aaaggccagt ggggcaccgt 240
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 ttcaaa 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Leu	Leu	Phe	Ser	Leu	Ile	Leu	Ala	Ile	Cys	Thr	Arg	Pro	Gly
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Phe	Leu	Ala	Ser	Pro	Ser	Gly	Val	Arg	Leu	Val	Gly	Gly	Leu	His	Arg
							20			25					30

Cys	Glu	Gly	Arg	Val	Glu	Val	Glu	Gln	Lys	Gly	Gln	Trp	Gly	Thr	Val
								35		40					45

Cys	Asp	Asp	Gly	Trp	Asp	Ile	Lys	Asp	Val	Ala	Val	Leu	Cys	Arg	Glu
								50		55					60

Leu	Gly	Cys	Gly	Ala	Ala	Ser	Gly	Thr	Pro	Ser	Gly	Ile	Leu	Tyr	Glu
								65		70		75		80	

Pro	Pro	Ala	Glu	Lys	Glu	Gln	Lys	Val	Leu	Ile	Gln	Ser	Val	Ser	Cys
								85		90					95

Thr	Gly	Thr	Glu	Asp	Thr	Leu	Ala	Gln	Cys	Glu	Gln	Glu	Glu	Val	Tyr
								100		105					110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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<400> 149
ttcagctcat cacccacc tgcc                                24

<210> 150
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 150
ggctcataca aaataccact aggg                                24

<210> 151
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 151
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt      50

<210> 152
<211> 1427
<212> DNA
<213> Homo sapiens

<400> 152
actgcactcg gtttatcgta ttgaattccc cggggatcct ctagagatcc ctgcaccc 60
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gaaggtgaag gccatggact tcatcaccc cacagccatc ctgcacctgc tgccggctg 180
cctggcgctc ttccgcctt tccggctgt gcagtgggtg cgcggaaagg cctacctgcg 240
aatgtgtgt gtggatca caggcgccac ctcaggctg ggcaaagaat gtgaaaagt 300
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gctcatcaga gaacttaccg cttctatgc caccaagggtg cagacacaca agcctactt 420
ggtacccctc gacccacag actctgggc catagttca gcagcagctg agatcctgca 480
gtgctttggc tatgtcgaca tacttgtca caatgtggg atcagctacc gtggtaccat 540
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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
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 20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala
 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 154
ggtgctaaac tggtgctctg tggc

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 155
cagggcaaga tgagcattcc

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 156		
tcatactgtt ccatctcgcc acgc	24	
<210> 157		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 157		
aatgggtgggg ccctagaaga gctcatcaga gaactcacccg cttctcatgc	50	
<210> 158		
<211> 1771		
<212> DNA		
<213> Homo sapiens		
<400> 158		
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cctcctgctt ctccccgttac tgatcgtctg ctcctctagag tccttcgtga agcttttat 180		
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tcataacctt gtggtagact gcagcaaccc agaagatatt tacagctctg caaaagaagg 420		
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<210> 159		

<211> 300
<212> PRT
<213> Homo sapiens

<400> 159
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Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
20 25 30
Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
35 40 45
Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
50 55 60
Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
65 70 75 80
Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
85 90 95
Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
100 105 110
Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
115 120 125
Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
130 135 140
Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
145 150 155 160
Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
165 170 175
Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
180 185 190
Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
195 200 205
Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
210 215 220
Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
225 230 235 240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
245 250 255

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<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
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Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85	90	95	
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100	105	110	
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115	120	125	
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130	135	140	
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145	150	155	160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165	170	175	
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180	185	190	
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195	200	205	
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215	220	
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245	250	255	
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260	265	270	
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275	280	285	
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295	300	
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325	330	335	
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340	345	350	

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgcca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgagggcttt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
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<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
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Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
 115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
 165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171
tggaaataccg cctcctgcag
<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172
cttctgcctt ttggagaaga tggc

20

24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
 ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

 <210> 174
 <211> 3106
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (1683)
 <223> a, t, c or g

 <400> 174
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 ttagtccag ggtggtgcca ctccagtaca agcgtgggg acctatcatt gccgtgcagg 660
 tggagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720
 cactggagga ccgtggcatt gtggaaactgc tcctgacttc agacaacaag gatggctga 780
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agccatggcc	catgtctgca	catccaggga	ggaggacaga	aggcccagct	cacatgtgag	2880
tcctggcaga	agccatggcc	catgtctgca	catccaggga	ggaggacaga	aggcccagct	2940
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gaagtgtgtc	caagtccgca	tttgagcctt	gttctggggc	ccagoccaac	acctggcttg	3060
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

222 (539)

<223> Any amino acid

<400> 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
 100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
120 125 130

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

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20					25				30					

Asp	Arg	Gly	His	Asp	Arg	Phe	Leu	Leu	Asp	Gly	Ala	Pro	Phe	Arg	Tyr
35				40					45						

Val	Ser	Gly	Ser	Leu	His	Tyr	Phe	Arg	Val	Pro	Arg	Val	Leu	Trp	Ala
50				55					60						

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65 70 75 80
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
 100 105 110
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
 115 120 125
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
 130 135 140
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
 145 150 155 160
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
 180 185 190
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
 195 200 205
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
 210 215 220
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
 225 230 235 240
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
 245 250 255
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
 260 265 270
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
 290 295 300
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
 305 310 315 320
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
 325 330 335
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178
tggctactcc aagaccctgg catg 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179
tggacaaatc cccttgctca gccc 24

<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180
gggcttcacc gaaggcagtgg acctttatcc tgaccacctg atgtccaggg 50

<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181
ccagctatga ctatgatgca cc 22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182
 tggcaccagg aatgggtttg gctc

24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt ccttgggac cttaacctcc

50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
 gcttgaaca cgtctgcaag cccaaagtgc agcatctgat tggttatgag gtatttgagt 60
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 gtgttatgg ctttatctgc ctctacactc tcttctgggtt attcaggata ctttgaagg 180
 aatattcttt cggaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240
 acgattttgc gttccttctt cacatggtag accagttatga ccagctatat tccaagcggtt 300
 ttgggtgtttt cttgtcagaa gtttgtaaaa ataaaacttag ggaaatttagt ttgaaccatg 360
 agtggacatt tggaaaactc aggccgcaca tttcacgcaa cggccaggac aagcaggagt 420
 tgcatctgtt catgctgtcg ggggtgcccgg atgctgtctt tgacccatcaca gacctggatg 480
 tgctaaagct tgaactaatt ccagaagcta aaattccctgc taagatttct caaatgacta 540
 acctccaaaga gctccaccc tcgcactgccc ctgcggaaaagt tgaacagact gcttttagt 600
 ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattccctg 660
 cctgggtgta tttgctcaaa aacccatcgag agttgtactt aataggcaat ttgaactctg 720
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcccacccctt aagattctcc 780
 acgtgaagag caatttgcacc aaagttccctt ccaacattac agatgtggct ccacatctta 840
 caaagtttagt cattcataat gacggcacta aactcttgggt actgaacagc cttaaagaaaa 900
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
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gcataaaagtt gaggactttg aatctggac agaactgcat cacctcaactc ccagagaaaag 1380
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 agggaaaggaa aaattataat cactaatctt ggttctttt aaattgttg taacttgat 1860
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 ttttctact aaaaaaaaaaaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
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Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
					20			25					30		

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
						35		40				45			

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
						50		55			60				

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
						65		70			75			80	

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
						85			90			95			

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
						100		105			110				

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
						115		120			125				

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
						130		135			140				

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
						145		150			155		160		

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
						165			170			175			

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
						180		185			190				

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
485 490 495

Phe Ala Asn Gly Ile
500

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 186
cctccctcta ttacccatgt c

21

<210> 187
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 187
gaccaacctt ctctggagttt gagg

24

<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 188
gtcactttat ttctctaaaca acaagctcgaa atccttacca gtggcag

47

<210> 189
<211> 2917
<212> DNA
<213> Homo sapiens

<400> 189
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actttttta ttctttttt tccatctctg ggccagtttgg gatccttagg ccgccttggg 120
aagacatgg tggtttacac acataaggat ctgtgtttgg ggtttttctt tcccccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtggcgtca gtgcttgct 240
gcacttatct gcctaggta atcgaagtct ttgcacctcc atacaatgt tatgcctgtc 300
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cacaaccagg acaagggtgtg gtgggccaag aacagccagg ccaaaccat tgccacggag 480
tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgcagtt tgattccctg 540
ccaccttgct gttgcgacat aaatgaggc ctctgagttt ggaaaggctc cttctcaaa 600
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgttgtgat gtgcaggcac 660
agaagaaaagg cacagctccc catcagttc atggaaaata actcagtgcc tgctgggaac 720
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tccaggatgc caaaggaaat gctacccctgt ggctacacat attatgaata aatgagggaa 2880
ggcctgaaag tgacacacag gcctgcgtt aaaaaaaaaaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565	570	575
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<210> 191		
<211> 21		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 191		
tctctattcc aaactgtggc g		
21		
<210> 192		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 192		
tttgatgacg attcgaaggt gg		
22		
<210> 193		
<211> 47		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 193		
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcac cctgagc		
47		
<210> 194		
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<212> DNA		
<213> Homo sapiens		
<400> 194		
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ctgctgtgc cggccgcgcgttcc cacagcgcca cgcgttcga ccccacctgg 180		

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 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu

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Leu Leu Leu Leu Pro Pro Pro Cys Pro Ala His Ser Ala Thr

20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
450 455 460

Asn Val Ile
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<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Dea

oli

<400> 196

<210> 197

23

<212> DNA

<213> Ar

<220>

<400> 187

ggatccatc

-218- 108

29

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 198
aacttgcagc atcagccact ctgc 24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 199
ttccgtgccc agttcggtt gcgagtggtt ctgggtgtat tggca 45

<210> 200
<211> 2372
<212> DNA
<213> Homo sapiens

<400> 200
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gtgttgcctc tcacttccat ctggaccacg aggctctgg tccaaggctc tttgcgtgca 240
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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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															30
20								25							

Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
															45
35								40							

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
															60
50								55							

Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
															80
65								70			75				

Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
															95
85								90							

Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
															110
100								105							

Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
															125
115								120							

Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
															140
130								135							

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 202
 gagctttcca tccaggtgtc atgc

 <210> 203
 <211> 22
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 203
      gtcagtgaca gtacctactc gg                                22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 204
      tggagcagga ggagtagtag tagg                                24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 205
      aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt   50

<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (973)
<223> a, t, c or g

<220>
<221> modified_base
<222> (977)
<223> a, t, c or g

<220>
<221> modified_base
<222> (996)
<223> a, t, c or g

<220>
<221> modified_base

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<222> (1003)

<223> a, t, c or g

<400> 206

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 ggaaactgccc gcccgtctgc cacggctctgc ccacccaacg cgaagacggt aaccctgtg 180
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 accgcagatc catcaactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
 ccaacacaat tctttcttc cgcttgata ttcgcattggg cctactttac atcacactct 360
 gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggcccttag tatataagg 420
 acttcaatga taaaaccatt gatgagaac tagaacggga caagagggtc acttggattg 480
 tggagttctt tgccaattgg tctaattact gccaattcatt tgccctatc tatgctgacc 540
 tctcccttaa atacaactgt acaggcataa attttggaa ggtggatgtt ggacgctata 600
 ctgatgttag tacgcggtaa aaagttagca catcaccctt caccaagcaa ctccctacc 660
 tgatcctgtt ccaaggtggc aaggaggca tgccggggcc acagattgac aagaaaggac 720
 gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
 tataccagcg ggccaagaaaa ctaatcaaagg ctggagacaa tatcccttag gggcgcctg 840
 tggcttcaac cccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
 actttggcag tgcttcctct cctgtcaatt ccaggctctt tccataacca caagccttag 960
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

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Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
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 275 280 285
 Asp Gly Glu Asn Lys Lys Asp Lys
 290 295
 <210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 208
 gcttggatat tcgcatgggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210
 aacagtggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211
 ccattgtatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
 ggacagtcg cgccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgcc 60
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 cccattgtctc ctgctgccccg gctcctacgg actgcccttc tacaacggct tctactactc 180
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr

1

5

10

15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp

20

25

30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys

35

40

45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala

50

55

60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser

65

70

75

80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala

85

90

95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe

100

105

110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr		
130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
305	310	315
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu		
325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
340	345	350
Gly Val Tyr Cys Tyr Arg Gln His		
355	360	
<210> 214		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

ttcccttgtg ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agccagttag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24

<210> 219
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 219
 gatgccacga tcgccaagg gggacagctc tttccgcctt ggaag 45

<210> 220
 <211> 1503
 <212> DNA
 <213> Homo sapiens

<400> 220
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 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
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Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

<400> 225

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44

<210> 226

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 226

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 aaa 2403

<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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			20				25					30			

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
	35					40					45				

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
	50					55					60				

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
65					70				75				80		

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
	85					90					95				

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
	100					105					110				

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
	115					120				125					

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
	130				135					140					

Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
145				150			155					160			

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
	165					170					175				

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
	180				185						190				

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
	195					200					205				

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
	210				215				220						

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
225				230				235			240				

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
	245					250					255				

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
 260 265 270
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
 290 295 300
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
 305 310 315 320
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480
 Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228
tggtctcgca caccgatc

18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca caggggag

18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc

18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatacgaa ttcccgcc

18

<210> 232

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232
 ttcctcaaga gggcagcc 18

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 233
 cttggcacca atgtccgaga ttcc 24

<210> 234
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 234
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<210> 235
 <211> 2586
 <212> DNA
 <213> Homo sapiens

<400> 235
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<210> 236
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 236
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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95

 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
 100 105 110

 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125

 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Gly Arg Arg Ser
 130 135 140

 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160

 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175

 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190

 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205

 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220

 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240

 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255

 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270

 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285

 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300

 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320

 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
 325 330 335

 Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
 340 345 350

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<212> DNA		
<213> Artificial Sequence		
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<210> 239		
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<223> Synthetic Oligonucleotide Probe		
<400> 239		
gcagagcgg aatgcggcgg ctgg		24
<210> 240		
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<223> Synthetic Oligonucleotide Probe		
<400> 240		
ttggcagctt catggagg		18
<210> 241		
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<223> Synthetic Oligonucleotide Probe		
<400> 241		
cctggcaaa aatgcaac		18

<210> 242
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 242
ctccagctcc tggcgcacct cctc

24

<210> 243
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 243
ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg

45

<210> 244
<211> 3679
<212> DNA
<213> Homo Sapien

<400> 244
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cacacataca ctttcctctc cttcactgaa gactcacagt cactcactct 200
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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly
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				20										30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
					35									45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
					50				55					60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
					65					70				75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
					80				85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
					95					100				105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
					110				115					120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
						125			130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
					140				145					150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser		
155	160	165
Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile		
170	175	180
Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met		
185	190	195
Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg		
200	205	210
Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu		
215	220	225
Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu		
230	235	240
Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg		
245	250	255
Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys		
260	265	270
Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu		
275	280	285
His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser		
290	295	300
Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu		
305	310	315
Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala		
320	325	330
Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn		
335	340	345
Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn		
350	355	360
Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys		
365	370	375
Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile		
380	385	390
Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg		
395	400	405
Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys		

410	415	420
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425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
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Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
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Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
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575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
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 Leu Pro Pro Leu Ser Gln Asn Ser
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 <210> 246
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 246
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 <210> 247
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 247
 aaacttgtcg atggagacca gctc 24

 <210> 248
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 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 248
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 <210> 249
 <211> 3401
 <212> DNA
 <213> Homo Sapien

 <400> 249
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catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200
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gcttccttct acatcagct agtcatcttc tacggcctca tctgcatgta 300
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<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile	1	5	10	15
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Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp	20	25	30
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg	35	40	45
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe	50	55	60
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr	65	70	75
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu	80	85	90
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Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His		
365	370	375
Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile		
380	385	390
Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu		
395	400	405
Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys		
410	415	420
Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe		
425	430	435
Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala		
440	445	450
Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln		
455	460	465
Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln		
470	475	480
Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile		
485	490	495
Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly		
500	505	510
Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp		
515	520	525
Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg		
530	535	540
Ala Asp Lys Glu Gln Ala		
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<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 252
gatggctagg ttctggaggt tctg 24

<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 253
caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

<400> 254
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<210> 255
<211> 452
<212> PRT
<213> Homo Sapien

<400> 255
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 35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
 50 55 60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
 65 70 75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
 80 85 90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
 95 100 105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
 110 115 120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
 125 130 135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
 140 145 150

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165

Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180

Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195

Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210

Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225

Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240

Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255

Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270

Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285

Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300

Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp 320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe 335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly 350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp 365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu 380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp 395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn 410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser 425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln 440	445	450
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<210> 256		
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<212> DNA		
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 <400> 256		
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
1					5				10				15	

Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
					20			25				30		

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
						35			40			45		

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
					50			55				60		

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
					65			70				75		

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
						80		85				90		

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
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 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
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 <211> 2427
 <212> DNA
 <213> Homo Sapien
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 aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln
1	5	10	15

Ser	Gly	Lys	Cys
Ser	Tyr	Pro	Glu

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35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly
				290					295				300	
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser
				305					310				315	
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp
				320					325				330	
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met
				335					340				345	
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp
				350					355				360	
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg
				365					370				375	
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly
				380					385				390	
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp
				395					400				405	
Tyr	Ile	Ser	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	
				410					415				420	
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Pro	His	
				425					430				435	
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440					445				450	
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455					460				465	
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470					475				480	
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485					490				495	
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln
				500					505				510	
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515					520				525	
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530					535				540	
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu
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Cys

<210> 260
 <211> 1638
 <212> DNA
 <213> Homo Sapien

<400> 260
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 taagggaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350
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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Leu
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Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
					20				25				30	

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
					35				40				45	

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
					50				55				60	

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
					65				70				75	

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
					80				85				90	

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
									95				100	

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
					110				115				120	

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
 290 295 300
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
 305 310 315
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
 320 325 330
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
 335 340 345
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
 350 355 360
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
 365 370 375
 Asn Tyr Leu Asp Cys Arg Glu Gly
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<210> 262

<211> 1378

<212> DNA

<213> Homo Sapien

<400> 262

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<210> 263  
<211> 317
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<210> 263
<211> 317
<212> PRT
<213> Homo_Sapiens

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
				20						25				30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40					45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50				55						60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65					70					75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80					85					90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95				100						105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110					115					120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125				130						135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140					145					150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155				160						165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
				170				175						180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
 185 190 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
 200 205 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
 215 220 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 245 250 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
 260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
 275 280 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
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Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

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<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA
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<220>
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<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
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<210> 268
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<400> 268
ggggattca ccctatgaca ttgcc 25

<210> 269
<211> 24
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<220>
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<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
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<220>
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<400> 270
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<210> 271
<211> 26
<212> DNA
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<400> 271
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<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
c a g c c t g c c a c a t g t g c 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
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<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
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<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
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<400> 275
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<210> 276
<211> 21
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcaggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gtcataaca gttcccttgc ccca 34

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282
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tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283
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gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100
atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
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ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggggagct gcacaacctc taccgggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
 ctggccgact tcgccaaggc ctacgcacgg cagtgcgtgt gggccacaa 250
 caaggagcgc gggcgccgagc gcgagaatct gttcgccatc acagacgagg 300
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
 tacaacctca ggcgcgccac ctgcagccca ggccagatgt gcggccacta 400
 cacgcagggtg gtatgggcca agacagagag gatcggtgt ggttccact 450
 tctgtgagaa gtcgcagggt gttgaggaga ccaacatcga attactggtg 500
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600
 tctgtgaacc catcggaaga ccggaaagatg ctcaggattt gccttacctg 650
 gtaactgagg ccccatcctt ccggcgact gaagcatcag actctaggaa 700
 aatgggtact ctttcttccc tagcaacggg gattccggct ttcttgtaa 750
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 gcctgcctc cttggatgag gagccagttt cttcccttcca atcgacccat 950
 gttccatatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
 caagggaaact cttcccttcca gcccaggagg aggctgaggc tgaggctgag 1100
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 gccaggtgag ctgcaggcca cactggacca cacggggcac acctccttcca 1200
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 caagccttagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350
 gcccctcttcca gggactactg ctccctgcctc ctctgggttt ggctggaatc 1400

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 ataaaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
									25					30

Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
									35					45

Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
									50		55			60

Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
									65		70			75

Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
									80		85			90

Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
									95		100			105

Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
									110		115			120

Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
									125		130			135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
 140 145 150
 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
 155 160 165
 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
 170 175 180
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
 200 205 210
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
 215 220 225
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
 230 235 240
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
 245 250 255
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
 260 265 270
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
 275 280 285
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
 290 295 300
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
 320 325 330
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
 335 340 345
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Ala Glu Ala Glu
 350 355 360
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
 380 385 390
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
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<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaactga 200
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 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250
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 ttttttaact ttgtttatg caaaaaagta tcttacgtaa attaatgata 3500
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 gaaaatgagt tactaaagca ttttaataa tacctgcctt gtaccatttt 3600
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 tgtcaatttg aa 3662

<210> 290
 <211> 1059
 <212> PRT
 <213> Homo Sapien

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 35 40 45
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
 50 55 60
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 65 70 75
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 80 85 90
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 95 100 105
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 110 115 120
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 125 130 135
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
 140 145 150
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
 155 160 165
 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
 170 175 180
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
 185 190 195
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
 200 205 210
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
 215 220 225
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
 230 235 240
 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
 245 250 255
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
 260 265 270
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
 275 280 285
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

290	295	300
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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg 320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala 335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn 350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys 365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys 380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln 395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly 410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp 425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala 440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser 455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu 470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln 485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu 500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn 515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn 530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg 545	550	555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
 560 565 570
 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
 575 580 585
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
 590 595 600
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
 605 610 615
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
 620 625 630
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
 635 640 645
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
 650 655 660
 Gly Gly Ser Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
 665 670 675
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 680 685 690
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
 695 700 705
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 710 715 720
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 725 730 735
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 740 745 750
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 755 760 765
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys
 770 775 780
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 785 790 795
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 800 805 810

Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	
															815
															820
															825
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	
															830
															835
															840
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	
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															850
															855
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	
															860
															865
															870
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	
															875
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Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	
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Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	
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Asp	Ala	Tyr	Ser	Ser	Phe	Gly	Gln	Pro	Ser	Asp	Cys	Gln	Pro	Arg	
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															1000
Ala	Phe	Tyr	Leu	Lys	Ala	His	Ser	Ser	Pro	Asp	Leu	Asp	Ser	Gly	
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															1015
															1020
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															1035
His	Ile	Cys	Thr	Phe	Lys	Gln	Thr	Leu	Glu	Asn	Tyr	Arg	Thr	Pro	
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<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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acacagggag cattcaagaa tgaataaac cagagttaga cccgcggggg 250
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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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									20			25		30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
									35			40		45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
									50			55		60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
									65			70		75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
									80			85		90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
									95			100		105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
									110			115		120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
									125			130		135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
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Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

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170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
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Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
350	355	360
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Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
410	415	420

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 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
 455 460 465
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
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 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
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 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
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 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
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 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
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 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
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 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
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 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
 575 580 585
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
 590 595 600
 Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn
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<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly

20

25

30

Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg

35

40

45

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys

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55

60

Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp

65

70

75

Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys

80

85

90

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu

95

100

105

Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser

110

115

120

Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu

125

130

135

Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu

140

145

150

Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro

155

160

165

Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr

170

175

180

Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu

185

190

195

Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys

200

205

210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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245	250	255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
 485 490 495
 Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
 500 505 510
 Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
 515 520 525
 Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
 530 535 540
 Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
 545 550 555
 Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
 560 565 570
 Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
 575 580 585
 His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
 590 595 600
 Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
 605 610 615
 Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
 620 625 630
 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
 635 640 645
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
 650 655 660
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
 665 670 675
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 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
 710 715 720
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
 725 730 735
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 740 745 750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
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 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 770 775 780
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 785 790 795
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
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 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
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 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 860 865 870
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
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<400> 296
cctaaaactga actggacca 19

<210> 297
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 297
ggctggagac actgaacct 19

<210> 298
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<220>
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<400> 298
acagctgcac agtcagaac agtg 24

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<400> 304
ccccatgtgt ccatgactgt tccc 24

<210> 305
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actccaagga aatcgatcc gttc 24

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<400> 309
gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien

<400> 310

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<400> 312
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<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<400> 313
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<210> 314
<211> 3003
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<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

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65 70 75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
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 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

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<210> 317
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<220>
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<400> 317
ttgcacttgtt aggacccacg tacg 24

<210> 318
<211> 50
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<210> 319
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<212> DNA

<213> Homo Sapien

<400> 319

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 aaaaaaaaaaa 2110

<210> 320
 <211> 450
 <212> PRT
 <213> Homo Sapien

<400> 320
 Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly
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 Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
 20 25 30
 Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
 35 40 45
 His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
 50 55 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Asp His Pro Glu		
440	445	450

<210> 321
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 321
gatcctgtca caaagccagt ggtgc 25

<210> 322
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 322
cactgacagg gttcctcacc cagg 24

<210> 323
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgc aaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatac 300

ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaaacttt ataagtgata 400

aagagtggaa gagtattgag cccgtttcat catggtttg tccaggttct 450

gttctgatga gtagtatgtc agcaactctt cagctatcta tgtggatcag 500

gacgtgccat aactactta ttgaagacct tggattgcca gtgtgggat 550

catatactgt ttttgctta gcaactctgt tttccggact gttatttagga 600

ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650

accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700

aaccttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750

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gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

aagattgatc atttgtttt gttgaagtg aactgtgact ttttgaata 950

ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn

20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly

35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln

50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp

65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly

80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His

95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys

110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile

125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser

140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys

155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser

170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu

185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys

200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

215 220 225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240
Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu
245 250 255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
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Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
tgaggtggc aagcgccgaa atg 23

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
tgcagggttc agtcttagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

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gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800
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 ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450
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gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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				20					25					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35				40					45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50				55				60		

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65				70				75		

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80				85				90		

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95				100				105		

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110				115				120		

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125				130				135		

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140				145				150		

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155				160				165		

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170				175				180		

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185				190				195		

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu	
				200				205				210		

Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg
215									220					225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His
230									235					240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu
245									250					255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu
260									265					270
Ala	Thr	Pro	Glu	Gly	Ile	Tyr	Glu	Arg	Pro	Val	Asp	Tyr	Leu	Pro
275									280					285
Glu	Arg	Asp	Val	Tyr	Glu	Ser	Leu	Cys	Arg	Gly	Glu	Gly	Val	Lys
290									295					300
Leu	Thr	Pro	Arg	Arg	Gln	Lys	Arg	Leu	Phe	Cys	Arg	Tyr	His	His
305									310					315
Gly	Asn	Arg	Ala	Pro	Gln	Leu	Leu	Ile	Ala	Pro	Phe	Lys	Glu	Glu
320									325					330
Asp	Glu	Trp	Asp	Ser	Pro	His	Ile	Val	Arg	Tyr	Tyr	Asp	Val	Met
335									340					345
Ser	Asp	Glu	Glu	Ile	Glu	Arg	Ile	Lys	Glu	Ile	Ala	Lys	Pro	Lys
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Leu	Ala	Arg	Ala	Thr	Val	Arg	Asp	Pro	Lys	Thr	Gly	Val	Leu	Thr
365									370					375
Val	Ala	Ser	Tyr	Arg	Val	Ser	Lys	Ser	Ser	Trp	Leu	Glu	Glu	Asp
380									385					390
Asp	Asp	Pro	Val	Val	Ala	Arg	Val	Asn	Arg	Arg	Met	Gln	His	Ile
395									400					405
Thr	Gly	Leu	Thr	Val	Lys	Thr	Ala	Glu	Leu	Leu	Gln	Val	Ala	Asn
410									415					420
Tyr	Gly	Val	Gly	Gly	Gln	Tyr	Glu	Pro	His	Phe	Asp	Phe	Ser	Arg
425									430					435
Arg	Pro	Phe	Asp	Ser	Gly	Leu	Lys	Thr	Glu	Gly	Asn	Arg	Leu	Ala
440									445					450
Thr	Phe	Leu	Asn	Tyr	Met	Ser	Asp	Val	Glu	Ala	Gly	Gly	Ala	Thr
455									460					465
Val	Phe	Pro	Asp	Leu	Gly	Ala	Ala	Ile	Trp	Pro	Lys	Lys	Gly	Thr
470									475					480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
ggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338
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<212> DNA
<213> Homo Sapien

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 ggggctcta tagggggag atttgaccgg caggcttctg cgagggctg 2350
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 aactctacca ccgctgccgc ctcagcaacc tggagggctt agggggccgt 2600
 gcccagctgg ctatggctt cttttagcag gagcaggcca atagcactta 2650
 gcccgcctgg gggccctaac ctcattacct ttcccttgc tgcctcagcc 2700
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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
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Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
									20			25		30

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
									35			40		45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
									50			55		60

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
									65			70		75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
									80			85		90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val		
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr		
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser		
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg		
155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile		
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu		
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala		
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly		
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg		
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro		
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly		
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu		
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu		
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr		
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr		
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val		
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu		
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
 365 370 375

 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
 380 385 390

 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
 395 400 405

 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
 410 415 420

 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
 425 430 435

 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
 440 445 450

 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
 455 460 465

 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
 470 475 480

 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
 485 490 495

 Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
 500 505 510

 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
 515 520 525

 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
 530 535 540

 Pro Phe Leu Gly Val Lys Ala Ala Ala Glu Leu Glu Arg Arg
 545 550 555

 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
 560 565 570

 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
 575 580 585

 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
 590 595 600

 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
 605 610 615

 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
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 <211> 1572
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 <213> Homo Sapien
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 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
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 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
 aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500
 ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550
 tttgttaaaa aaggatccat cacagcctt ctatcttaggc cacactataa 600
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
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 gtaactacat atccaataaca gctgtatgtt tcttttctt ttctaatgg 1150
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaatga 1200
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 tgtgtgttcc ctttacttctt aatactgattt tatgttctaa gcctccccaa 1500
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<210> 341
 <211> 318
 <212> PRT
 <213> Homo Sapien

<400> 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
					20				25				30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
					35				40				45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
					50				55				60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
					65				70				75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
					80				85				90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
					95				100				105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
					110				115				120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
					125				130				135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
					140				145				150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
					155				160				165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
					170				175				180	
Val	Gly	Met	Glu	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	
					185				190				195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
					200				205				210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
					215				220				225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
					230				235				240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
					245				250				255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys